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Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/437,450

11/10/99

FREEDMAN

J

1579-315

NIXON & VANDERHYE PC  
1100 NORTH GLEBE ROAD  
8TH FLOOR  
ARLINGTON VA 22201

HM22/0530

EXAMINER

PARAS JR, P

ART UNIT

PAPER NUMBER

1632

DATE MAILED:

05/30/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office

Address: ASSISTANT COMMISSIONER FOR PATENTS

Washington, D.C. 20231

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT

PAPER

11

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner of Patents and Trademarks

**Sequence Compliance**

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

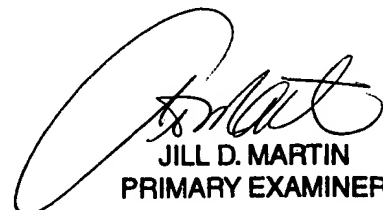
APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner(s) should be directed to Peter Paras, Jr., whose telephone number is 703-308-8340. The examiner can normally be reached Monday-Friday from 8:30 to 4:30 (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Karen Hauda, can be reached at 703-305-6608. Papers related to this application may be submitted by facsimile transmission. Papers should be faxed via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The CM1 Fax Center numbers are (703)308-4242

Inquiries of a general nature or relating to the status of the application should be directed to Kay Pinkney whose telephone number is (703) 305-3553.

Peter Paras, Jr.  
Art Unit 1632

  
JILL D. MARTIN  
PRIMARY EXAMINER

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

# Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/437,450

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

JAN 23 2001

TECH CENTER 1600/2900

- 1 ☐ Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)  
Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)  
Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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Does Not Comply  
Corrected Diskette Needed

pp 1-2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/437,450

DATE: 01/09/2001  
TIME: 07:40:51

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\01092001\I437450.raw

3 <110> APPLICANT: FREEDMAN, JONATHAN H.  
4 LIAO, VIVIAN H.C.  
6 <120> TITLE OF INVENTION: STRESSOR REGULATOR GENE  
8 <130> FILE REFERENCE: 1579-315  
10 <140> CURRENT APPLICATION NUMBER: 09/437,450  
11 <141> CURRENT FILING DATE: 1999-11-10  
13 <150> PRIOR APPLICATION NUMBER: 60/109,281  
14 <151> PRIOR FILING DATE: 1998-11-20  
16 <160> NUMBER OF SEQ ID NOS: 72  
18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

1279 <210> SEQ ID NO: 72  
1280 <211> LENGTH: 10  
1281 <212> TYPE: DNA  
1282 <213> ORGANISM: Artificial Sequence  
1284 <220> FEATURE:  
1285 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe  
1287 <400> SEQUENCE: 72  
1288 ggtactaagc 10

E--> 1292 484138

Delete extraneous numerals at the  
end of the file. They are causing an  
invalid base count for sequence #72.

<210> 46  
 <211> 13322  
 <212> DNA  
 <213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence: Probe

<400> 46  
 grhttwvnc hnnngvnb anknpnks archhtmsnc nmatnsct ggtactccac 60  
 acggacaaat acatttagtt ttacaagccg ccacgcgaca cgcaacggcc gtaaactctac 120  
 ccaagggtaca acaacaacat gtcaagcaca gacccaatc ttatttggtc ggaaggatgg 180  
 cctctactgt agtaatcgac aattggactc ttatccaccg gatcacttaa cctattttga 240  
 tattaatatg cctgattggg gatcacaggg ttgcccga aatgtaatta tgaactgaat 300  
 tcgaaatgta ttataaatt agtttttatt ggsnegcaa gtgcggagac aaatgtgaat 360  
 gcagtggaga caagtgttgt gagaagtact gctgtgagga ggccagtgg aaaaatgct 420  
 gtccagctgg atgtaaggga gactgcaagt gtgcaaactg tcattgtgca gagcagaagc 480  
 agtgcgagac aagaccatc aacaccaggg aactgctgcg gctcattaaa atgtttcaga 540  
 gttgaatcta sncttagcaa gtgcggagac aaatgtgaat gcagtggaga caagtgttgt 600  
 gagaagtact gctgtgagga ggccagtgg aaaaatgct gtccagctgg atgtaaggga 660

Sequence 46 is missing the mandatory  
 <220> to <223> features to explain the  
 "n's" in the sequence. (See #10 on the  
 Error Summary Sheet.) Sequence 46  
 is only partially shown here, but contains  
 "n's" throughout its length.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/437,450

DATE: 01/09/2001  
TIME: 07:40:52

Input Set : A:\Sequence Listing.txt  
Output Set : N:\CRF3\01092001\I437450.raw

L:736 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:736 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:736 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46  
L:741 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:741 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
M:340 Repeated in SeqNo=46  
L:745 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:745 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:748 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:748 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:752 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:752 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:756 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:756 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:760 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:760 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:763 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:763 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:771 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:771 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:774 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:774 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:777 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:777 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:781 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:781 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:789 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:789 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:799 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:799 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:802 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:805 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:805 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:810 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:810 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:813 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:813 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:815 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:815 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:820 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:820 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46

VERIFICATION SUMMARY DATE: 01/09/2001  
PATENT APPLICATION: US/09/437,450 TIME: 07:40:52

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\01092001\I437450.raw

L:824 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:824 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:830 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46  
L:830 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46  
L:1292 M:254 E: No. of Bases conflict, LENGTH:Input:484138 Counted:10 SEQ:72